



Figure 1A

1 GGAAGTCAGCAGCGCTTGGGAGGGGTGGCGGGGGAATAGCGGGGCAGC
51 AGCCCCAGCCCTCAGAGACAGACAGAAAGGAGGGAGGGGTGCTGG
101 GGGGACAGCCCCCACCATTCTTACCGCTATGGGCCCAACCTCCCACTCC
151 CACCTCCCCCTCATCGGCCGGGCTAGGACACCCCCCAATCCCCGTGCCCC
201 CCTTGGCACCGACACCCCCGACAGACAGAGACACAGCCATCCGCCACCA
251 CCGCTGCCGAGCCTGGCTGGGAGGGGCCAGCCCCCAGGCCCTAC
301 CCCTCTGAGGTGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTG CTC TTC C
Met Leu Leu Leu Phe Leu Leu Leu Phe L
20
10
380 TG CTG CCC ACC CTG TGG TTC TGC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys
30

Figure 1B

418 TAC TTC TTC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

70

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

80

Figure 1C

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G

90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
In Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu

100

643 GAT CTG CTT GGG ATG ATG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C

120

110

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly

130

Figure 1D

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA GGA GTC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P

140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val

150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V

170

160

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His

180

Figure 1 E

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H

190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile

200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G

220

210

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val

230

Figure 1F

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A

240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met

250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G

270

260

1130 GT GGT GGT GAC TAT CTG AAG AAG CCT GGG GGC GGT GGG
ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCATCTTCTCTCCC

1216 CACACCTACCCACCCAGTGGGCCCTGAGCAGGGCCAAACCCTCTTCTCTT

1266 GTCTCCCCCTCTCCCCACTTATTCTCTCTCTTGGAACTTCAACTTCTGAA

Figure 1G

1316 GTGAATGTGGATACAGGCCACTCCTGCCCCCTCTTGGCCCCCATCCATGG
1366 ACTCTTGCCCTCGGTGCAGTTTCCACTCTTGACCCCCACCTCCTACTGTCT
1416 TGTCTGTGGACAGTTGCCCTCCCCCTCATCTCCAGTGACTCAGCCCTACAC
1466 AAGGAGGGGAACATTCCATCCCCAGTGGAGTCTCTCCTATGTGTCTT
1516 CTCTACCCCTCTACCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGA
1566 ACAAAATCCCCCCCACCTCCAAGTCCATGGATTCAATGGACTCATCCATT
1616 TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAGCTGATACCTGAAGCACT
1666 CCCAGGCTCATCCTGGGAGCTTTCCCTCAGCACCTTCACCTTCCCCTCCCAG
1716 TGTAGCCTCCTGTCAGTGGGGCTGGACCCCTTCTAATTCAGAGTCTCAT
1766 GCCTGCCCTTGCCCAAGATGCCCAAGGTCGTGCACTCTCTGGGATACCAGT
1816 TCAGTCTCCACATTTCTGGTTTCTGTGTCCCCCATAGTACAGTTCTTCAGTG
1866 GACATGACCCCAACCAGCCCCCTGCAGCCCTGCTGACCATCTCACCAGAC
1916 ACAAGGGGAAGAAGCAGACATCAGGTGCTGCACTCACTTCTGCCCCCTGG
1966 GGAGTTGGGAAAGGAACCAACCCCTGGCTGGAGGGGATAGGAGGCTTTT

Figure 1H

2016 AATTATTCTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTTC
2066 TTTCTTCCGTGGTCATTAGCCACTCCCTGCCCTCTCACTCCAGACCTGTT
2116 CCCACAAC TGGGAGGTAGGCTGGGAGCAAAAGGAGAGGGTGGGACCCAG
2166 TTTTGGCGTGGTTGGTTTATTATTAATCTGGATAACAGCAAAAACCTG
2216 AAAATAAGAGAGAGAGAAAAA

Figure 2 A

Human LPAAT	1	MDLWPGAWM-	10	20	30	40	50
Yeast LPAAT	1	MSV-IGRFLY	YLRSVL-VVL	AL-AG-----	LL-LLELLPT	LWFCSPSAKY	F-----FKMA
E.coli LPAAT	1	M-----	LYIF	RL-IITVIYS	ILVCVFGSIY	-----	-----G
Maize LPAAT	1	MAI-----	PLVLVVL	PLGLLFLLSG	LIVNAIQAVL	FVTIRPFSSKS	-----
Human LPAAT	51	FYNGWILFLA	VLAIPVCAVR	GRNVENMKIL	RLMLLHIKYL	-YGIRVEVRG	-----
Yeast LPAAT	51	FY-----G	VIASILCTLI	GKQHLAQWIT	ARCFYHVMKL	MLGLDV---K	-----
E.coli LPAAT	51	-----	CLFS	PRNPKHVATF	GHMFGRLAPL	-FGLKVECRK	-----
Maize LPAAT	51	FYRRINRFLA	EL-----	-----L	WLQLVWVVDW	WAGVKVQLHA	-----
Human LPAAT	101	AHFE-PPSQ-	PYVVVSNHQ	SSLDLLGMME	VL--PGRC--	-VPI-AKREL	-----
Yeast LPAAT	101	VUGE-ENLAK	KPYIMIANHQ	STLDIFMLGR	IF--PPGCT-	---VTAKKSL	-----
E.coli LPAAT	101	PTDA-ESYG-	NAIYIANHQ	NNYDMVTASN	IVQ-PP----	TVTIV-GKKSL	-----
Maize LPAAT	101	DEETYRSMGK	EHALIISNHR	SDIDWL-IGW	ILAQRSGCLG	STLAVMKKSS	-----
Human LPAAT	151	LWAGSAGLAC	W---LAGVIF	IDRKRTGDAL	SVMSEVAQTL	LTQDVRVWV-	-----
Yeast LPAAT	151	KYVPFLG---	WFMAISGTYF	LDRSKRQEI	DTLNKGLENV	KKNKRALWV-	-----
E.coli LPAAT	151	LWIPFFGQLY	W---LTGNLL	IDRNNRTKAH	GTIAEVVNHF	KKRRISIMW-	-----
Maize LPAAT	151	KFLPVGWSM	WF---AEYLE	LEERS-WAKDE	KTLKWGLQRL	KDFPRPFWLA	-----
Human LPAAT	201	FPEGTRNHN	GS-----	-----	MLPFKRGAFH	LAVQAQVPIV	-----
Yeast LPAAT	201	FPEGTRSYT	SEL-----	-----T	MLPFKKGAFH	LAQQGKIPIV	-----
E.coli LPAAT	201	FPEGTRSRG	RGL-----	-----	-LPFKTGAFH	AAIAAGVPIL	-----
Maize LPAAT	201	LFVEGTRFTP	AKLLAAQEYA	ASQGLPAPRN	VLIPTKGFV	SAVSIMRDFV	-----

Figure 2 B

Human LPAAT	251	<u>P</u> <u>I</u> <u>V</u> <u>M</u> <u>S</u> <u>S</u> <u>Y</u> <u>Q</u> <u>D</u> <u>F</u>	<u>Y</u> <u>C</u> <u>K</u> <u>K</u> <u>E</u> <u>R</u> <u>R</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>Q</u> <u>C</u> <u>Q</u> <u>V</u> <u>R</u> <u>V</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>P</u> <u>T</u> <u>E</u> <u>G</u> <u>L</u> <u>T</u> <u>P</u> <u>D</u> <u>D</u>	<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>A</u> <u>D</u> <u>R</u>
Yeast LPAAT	251	<u>P</u> <u>V</u> <u>V</u> <u>S</u> <u>N</u> <u>T</u> <u>S</u> <u>T</u> <u>L</u>	<u>V</u> <u>S</u> <u>P</u> <u>K</u> <u>Y</u> <u>G</u> <u>V</u> <u>F</u> <u>N</u> <u>R</u>	<u>G</u> <u>C</u> <u>M</u> <u>I</u> <u>V</u> <u>R</u> <u>I</u> <u>L</u> <u>K</u> <u>P</u>	<u>I</u> <u>S</u> <u>T</u> <u>E</u> <u>N</u> <u>L</u> <u>T</u> <u>K</u> <u>D</u> <u>K</u>	<u>I</u> <u>G</u> <u>E</u> <u>F</u> <u>A</u> <u>E</u> <u>K</u>
E.coli LPAAT	251	<u>P</u> <u>V</u> <u>C</u> <u>V</u> <u>S</u> <u>T</u> <u>S</u> <u>N</u> <u>K</u>	<u>I</u> <u>--</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>L</u> <u>H</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>Q</u> <u>Y</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u>
Maize LPAAT	251	<u>P</u> <u>A</u> <u>I</u> <u>Y</u> <u>D</u> <u>T</u> <u>--</u> <u>V</u>	<u>I</u> <u>V</u> <u>P</u> <u>K</u> <u>D</u> <u>S</u> <u>P</u> <u>Q</u> <u>P</u> <u>T</u>	<u>M</u> <u>L</u> <u>R</u> <u>I</u> <u>L</u> <u>K</u> <u>G</u> <u>Q</u> <u>S</u> <u>S</u>	<u>V</u> <u>I</u> <u>H</u> <u>V</u> <u>R</u> <u>M</u> <u>K</u> <u>R</u> <u>H</u> <u>A</u>	<u>M</u> <u>S</u> <u>E</u> <u>M</u> <u>P</u> <u>K</u> <u>S</u> <u>D</u> <u>E</u> <u>D</u>
		310	320	330	340	350
Human LPAAT	301	-----	<u>V</u> <u>R</u> <u>H</u> <u>S</u> <u>M</u> <u>L</u> <u>T</u> <u>V</u> <u>-</u> <u>F</u>	<u>R</u> <u>E</u> <u>I</u> <u>S</u> <u>T</u> <u>D</u> <u>G</u> <u>R</u> <u>G</u> <u>G</u>	<u>G</u> <u>D</u> <u>Y</u> <u>L</u> <u>K</u> <u>K</u> <u>P</u> <u>G</u> <u>G</u> <u>G</u>	<u>G</u> <u>*</u>
Yeast LPAAT	301	-----	<u>V</u> <u>R</u> <u>D</u> <u>Q</u> <u>M</u> <u>V</u> <u>D</u> <u>T</u> <u>-</u> <u>L</u>	<u>K</u> <u>E</u> <u>I</u> <u>G</u> <u>Y</u> <u>S</u> <u>P</u> <u>A</u> <u>I</u> <u>N</u>	<u>D</u> <u>T</u> <u>T</u> <u>L</u> <u>P</u> <u>P</u> <u>Q</u> <u>--</u>	-----
E.coli LPAAT	301	-----	<u>C</u> <u>R</u> <u>S</u> <u>I</u> <u>M</u> <u>E</u> <u>Q</u> <u>K</u> <u>-</u> <u>I</u>	<u>A</u> <u>E</u> <u>L</u> <u>D</u> <u>K</u> <u>E</u> <u>V</u> <u>A</u> <u>E</u> <u>-</u>	-----	<u>R</u> <u>E</u> <u>A</u> <u>A</u> <u>G</u> <u>K</u> <u>V</u> <u>*</u>
Maize LPAAT	301	<u>V</u> <u>S</u> <u>K</u> <u>W</u> <u>C</u> <u>K</u> <u>D</u> <u>I</u> <u>F</u> <u>V</u>	<u>A</u> <u>K</u> <u>D</u> <u>A</u> <u>L</u> <u>L</u> <u>D</u> <u>K</u> <u>H</u> <u>L</u>	<u>A</u> <u>T</u> <u>G</u> <u>T</u> <u>F</u> <u>D</u> <u>E</u> <u>E</u> <u>I</u> <u>R</u>	<u>P</u> <u>I</u> <u>G</u> <u>R</u> <u>P</u> <u>V</u> <u>K</u> <u>S</u> <u>L</u> <u>L</u>	<u>V</u> <u>T</u> <u>L</u> <u>F</u> <u>W</u> <u>S</u> <u>C</u> <u>L</u> <u>L</u> <u>L</u>
		360	370	380	390	400
Human LPAAT	351
Yeast LPAAT	351	-- <u>A</u> <u>I</u> <u>E</u> <u>Y</u> -- <u>A</u>	<u>A</u> <u>L</u> -- <u>Q</u>	<u>H</u> <u>D</u> <u>K</u> <u>V</u> <u>N</u> <u>K</u> <u>K</u> <u>I</u> <u>K</u>	<u>N</u> <u>E</u> <u>P</u> <u>V</u> <u>P</u> <u>S</u> <u>V</u> <u>S</u> <u>I</u> <u>S</u>	<u>N</u> <u>D</u> <u>V</u> <u>N</u> <u>T</u> <u>H</u> <u>N</u> <u>E</u> <u>G</u> <u>S</u>
E.coli LPAAT	351
Maize LPAAT	351	<u>F</u> <u>G</u> <u>A</u> <u>I</u> <u>E</u> <u>F</u> <u>F</u> <u>K</u> <u>W</u> <u>T</u>	<u>Q</u> <u>L</u> <u>L</u> <u>S</u> <u>T</u> <u>W</u> <u>R</u> <u>G</u> <u>V</u> <u>A</u>	<u>F</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>A</u> <u>L</u> <u>V</u> <u>T</u>	<u>G</u> <u>V</u> <u>M</u> <u>H</u> <u>V</u> <u>F</u> <u>I</u> <u>M</u> <u>F</u> <u>S</u>	<u>Q</u> <u>A</u> ----- <u>E</u> <u>R</u> <u>S</u>
		410	420	430	440	450
Human LPAAT	401
Yeast LPAAT	401	S----- <u>V</u>	<u>K</u> <u>K</u> <u>M</u> <u>H</u> <u>*</u>
E.coli LPAAT	401
Maize LPAAT	401	<u>S</u> <u>S</u> <u>A</u> <u>R</u> <u>A</u> <u>A</u> <u>R</u> <u>N</u> <u>R</u> <u>V</u>	<u>K</u> <u>K</u> <u>E</u> <u>*</u>

Figure 3A

10	20	30	40	50	60
GGAGCGAGCT	GGCGGCGCCG	TCGGGCGCCG	GGCCGGGCCA	TGGAGCTGTG	GCCGTGTCTG
70	80	90	100	110	120
GGCGGCGGC	TGCTGTTGCT	GCTGCTGCTG	GTGCAGCTGA	GCCGCGCGGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAGGTGC	CCCTGTACTG	CGCGCTGTGC	TTCACGGTGT	CCGCCGTGGC	CTCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGCGG	CCGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGCG	CAGGCTGCAG
310	320	330	340	350	360
GAGGCCCGTC	CCTGTGTTCAT	CGTCTCCAAC	CACCAGAGCA	TCCTGGACAT	GATGGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TTCCGGAGCG	CTGCGTGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGGC	GTCCTTCTTCA	TCAACCGGCA	GCGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACCTGGGC	GAGCGCATGG	TCAGGGAGAA	CCTCAAAGTG

Figure 3B

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAACGAC	AATGGGGACC	TGCTGCCCTTT	TAAGAAGGGC
610	620	630	640	650	660
GCCTTCTACC	TGGCAGTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTA	CTCTTCCCTC
670	680	690	700	710	720
TCCTCCTTCT	ACAACACCAA	GAAGAAAGTTC	TTCACCTTCAG	GAACAGTCAC	AGTGCAGGTG
730	740	750	760	770	780
CTGGAAGCCA	TCCCCACCAG	CGGCCTCACT	GCGGCGGACG	TCCCTGGGCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCGGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGGCA	GAGGGACTC	CTCCCCGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCCGGAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGCCCTT	GGTGTCCCCCT	GCAGGGGGCT	CAGCTGGACC

Figure 3C

1090	1100	1110	1120	1130	1140
CTCCCCGGC	TCGAGGCAG	GGA CTGCGC	CCACGGCACC	TCTGGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCCGCTGGT	GGGCTGAGCC	ACAAGGCCCC	CGATGGCCCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCAGACT	CACGCACCCCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGGAA	TCGGGGCCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGGG	GTCAGCACTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTTTT	ATAAACACAC	TCTTGGA AAA	AAAAAAA AAA	AAAAAAA AAA
1390	1400	1410	1420	1430	1440
AAA.....

Figure 4 A

10	20	30	40	50
GGAGCGAGCTGGCGCGCGTGGCGCGCGCGCGGCC	ATG	GAG	CTG	TGG
	Met	Glu	Leu	Trp
				Pro
60	70	80	90	
TGT CTG GCC GCG GCG CTG CTG TTG CTG CTG CTG	CTG	GAG	CTG	CAG
Cys Leu Ala Ala	Leu	Leu	Leu	Gln
				Leu
				20
100	110	120	130	140
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC	CTG	TAC	TGC	GCG
Ser Arg Ala Ala	Glu	Phe	Tyr	Ala
				30
150	160	170	180	
CTG TGC TTC ACG GTG TCC GCC GTG GCC TCG CTC	GTC	TGC	CTG	CTG
Leu Cys Phe Thr	Val	Ser	Ala	Val
				50
190	200	210	220	230
TGC CAC GGC GGC CCG ACG GTG GAG AAC ATG AGC	ATC	ATC	ATC	GGC
Cys His Gly Gly	Arg	Thr	Val	Glu
				60
				Trp

Figure 4B

240	TTC GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC CGC TTC GAG GTG	250	260	270	
	Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val	70		80	
280		290	300	310	320
	CGG GAC CCG CGC AGG CTG CAG GAG GCC CGT CCC TGT GTC ATC GTC				
	Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val			90	
330		340	350	360	
	TCC AAC CAC CAG AGC ATC CTG GAC ATG ATG GGC CTC ATG GAG GTC				
	Ser Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val				110
		100			
370		380	390	400	410
	CTT CCG GAG CAG TGC GTG CAG ATC GCC AAG CGG GAG CTC CTC TTC				
	Leu Pro Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Phe			120	
420		430	440	450	
	CTG GGG CCC GTG GGC CTC ATC ATG TAC CTC GGG GGC GTC TTC TTC				
	Leu Gly Pro Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe				140
		130			
460		470	480	490	500
	ATC AAC CCG CAG CGC TCT AGC ACT GCC ATG ACA GTG ATG GCC GAC				
	Ile Asn Arg Gln Arg Ser Thr Ala Met Thr Val Met Ala Asp				150

Figure 4C

510	CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT	530	540
	Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr		170
	160		
550	560	570	580
	CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CTG CCT TTT AAG		590
	Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys		180
	600	610	620
	AAG GGC GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC		630
	Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val		200
	190		
640	650	660	670
	CCC GTG GTG TAC TCT TCC TTC TCC TCC TTC TAC AAC ACC AAG AAG		680
	Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys		210
	700	710	720
690	AAG TTC TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC		
	Lys Phe Phe Thr Ser Gly Thr Val Thr Val Gln Val Leu Glu Ala		230
	220		

Figure 4D

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730      740      750      760      770
ATC CCC ACC AGC GGC CTC ACT GCG GCG GAC GTC CCT GCG CTC GTG
Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val
240

780      790      800      810
GAC ACC TGC CAC CGG GCC ATG AGG ACC ACC TTC CTC CAC ATC TCC
Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe Leu His Ile Ser
250      260

820      830      840      850      860
AAG ACC CCC CAG GAG AAC GGG GCC ACT GCG GGG TCT GGC GTG CAG
Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln
270

870      880      890      900      910      920
CCG GCC CAG TAG CCCAGACCAGGCGGCGATGACCTGGGGAGGCGAGGTGGAAGC
Pro Ala Gln ***

930      940      950      960      970      980
CGATGGCTGGAGGATGGGCAGAGGGGACTCCTCCCGGCTTCCAAATACCACTCTGTCCGG

990      1000      1010      1020      1030      1040
CTCCCCCAGCTCTCACTCAGCCCGGGAAGCAGGAAGCCCTTCTGTCACTGGTCTCAGAC
1050      1060      1070      1080      1090      1100
ACAGGCCCTGTGTCCCCTGCAGGGGGCTCAGCTGGACCCCTCCCGGGCTCGAGGGCAG
```

Figure 4E

1110	1120	1130	1140	1150	1160
	GGACTCGCGCC	CACGGCACCTCTGGNGCTGGNTGATAA	GATGAGGCTTGC	GGCTGTG	
1170	1180	1190	1200	1210	1220
	GCCCGCTGGTGGCTGAGCCACAAGCCCCCGATGGCC	CAGGAGCAGATGGGAGGACCCC			
1230	1240	1250	1260	1270	1280
	GAGGCCAGGAGTCCCAGACTCACGCACCCCTGGGCC	CACAGGAGCCGGGAATCGGGG	CGCTG		
1290	1300	1310	1320	1330	1340
	CTGCTCCTGCTGGCCTGAAGAACTCTGTGGGT	CAGCACTGTACTCCGTTGCTTTT			
1350	1360	1370	1380		
	ATAAACACACTCTTGGAAAA	AAAAAAAAAAAA			

Figure 5 A

Alignment of LPAAT Sequences.

Human LPAAT-β	1	10	20	30	40	50
Human LPAAT-α	1	---	---	MEL WPC	---	LA AALLLLLV
Yeast LPAAT	1	---	---	MDL WPGAWMLLL	IFLLFLFP	---
E.coli LPAAT	1	---	---	MSV	--IGRFLLYL	RSVLWLALA
H.influenzae	1	---	---	---	---	---
S.typhimurium	1	---	---	---	---	---
L.douglasi	1	MAKRTSS-L	RNR	---	RQLKP AVAATAD--D	DKDGVFHV--
C. nucifera	1	MDASCASSFL	RCRCLESCFK	ASFGMSQPKD	AAGQPSRRPA	DADDFIVDD
Human LPAAT-β	51	QL	---	SRAAE FYAKVAL-YC	ALCFTVSAVA	SLVCLLCHGG RTVENM-SII
Human LPAAT-α	51	TLWFCS	PSAK YFFKMAF-YN	GWILFLAVLA	IPVCAV--RG	RNVENM-KIL
Yeast LPAAT	51	G	---	CG	---	FY
E.coli LPAAT	51	---	---	MLYI	FRLLIVTVYS	ILVC
H.influenzae	51	---	---	MLKL	LRIFLMLICC	ILIC
S.typhimurium	51	---	---	MLYI	FRLLIVTVYS	ILVC
L.douglasi	51	---	---	LLSC	FKIFVCFEFT	VLIITAVANG
C. nucifera	51	DRWTFVILSV	VRIACFL	---	SMWTTIVN	MIMILLPWP YARIRGNLY

Figure 5 B

	110	120	130	140	150
Human LPAAT- β	101 <u>GMFVRSFKY</u> - --FYGLRFEV <u>RDPRLQEAR</u> <u>PCVIVSNHQ</u> <u>SLDILGMMEV</u>				
Human LPAAT- α	101 <u>RLMLIHICY</u> - --LYGIRVEV <u>RGAHFFPSQ</u> <u>PVWVSNHQ</u> <u>SILDILGMMEV</u>				
Yeast LPAAT	101 <u>CFY-HVMKL</u> - --MLGLDVKV <u>VGEENAK-K</u> <u>PYIMIANHQ</u> <u>TLDIFMIGRI</u>				
E.coli LPAAT	101 <u>GHMFGRL</u> --- <u>APLFLGLKVEC</u> <u>RKPTDAESYG</u> <u>NAIYIANHQ</u> <u>NYDMVTA SNI</u>				
H.influenzae	101 <u>ARWFGRL-FT</u> <u>YPLFLGLKVEH</u> <u>RIPQDQKQIS</u> <u>RAIYIGNHQ</u> <u>NYDMVT ISYM</u>				
S.typhimurii	101 <u>GHMFGRL-FT</u> <u>APLFLGLKVEC</u> <u>RKPADAENYG</u> <u>NAIYIANHQ</u> <u>NYDMVTAANI</u>				
L.douglassi	101 <u>GHIIGGLV</u> -- <u>IWIYGIPIKI</u> <u>QGSEHIKKRA</u> <u>IFTYISNHAS</u> <u>PIDAFVFMWL</u>				
C. nucifera	101 <u>GHVTGRMLFT</u> <u>MWILGNPITI</u> <u>EGSEFSNTRA</u> <u>I--YICNHAS</u> <u>LVDIFLIMWL</u>				
	160	170	180	190	200
Human LPAAT- β	151 <u>LPERCVOIAK</u> <u>RELLFLGPV</u> - <u>GLIMVLGV</u> <u>FFINRQSS</u> <u>AMT--VMALL</u>				
Human LPAAT- α	151 <u>LPGRCPPIAK</u> <u>RELLWAGSA</u> - <u>GLACWLAGV</u> <u>IFIDRKRTGD</u> <u>AIS--VMSEV</u>				
Yeast LPAAT	151 <u>FPPGCTVTAK</u> <u>KSLKVVPFL</u> - <u>GWFMALSGT</u> <u>YFLDRSKRQE</u> <u>AID--TINKG</u>				
E.coli LPAAT	151 <u>VQPPTVTGCK</u> <u>KSLWIPIPF</u> - <u>GQLYWL TGN</u> <u>LLIDRNNRTK</u> <u>AHG--TIAEV</u>				
H.influenzae	151 <u>VQPRIVSVCK</u> <u>KSLWIPIFFF</u> <u>TGILYWVTGN</u> <u>IFLDRENRTK</u> <u>AHN--TMSQL</u>				
S.typhimurii	151 <u>VQPPTVTGCK</u> <u>KSLWIPIFFF</u> <u>TGQLYWL TGN</u> <u>LLIDRNNRAK</u> <u>AHS--TIAAV</u>				
L.douglassi	151 <u>APIGTGVAK</u> <u>KEVIWYPILG</u> <u>Q--LYTLAH</u> <u>IRIDRSNPAA</u> <u>AIQSFTMKEA</u>				
C. nucifera	151 <u>IPKGTVTIAK</u> <u>KEIWIYPLEG</u> <u>QFTLYVLANH</u> <u>QRIDRSNPFA</u> <u>AI ES--IKEV</u>				

Figure 5C

	210	220	230	240	250	
Human LPAAT-β	201	<u>GERMREN</u> <u>LK</u>	<u>VW</u> <u>I</u> <u>Y</u> <u>PE</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>D</u> <u>N</u> <u>G</u> <u>D</u> <u>L</u> <u>-</u> <u>L</u> <u>P</u> <u>F</u>	<u>KK</u> <u>G</u> <u>A</u> <u>F</u> <u>Y</u> <u>L</u> <u>-</u> <u>A</u>	<u>V</u> <u>O</u> <u>A</u> <u>Q</u> <u>V</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>V</u>
Human LPAAT-α	201	<u>AQ</u> <u>T</u> <u>L</u> <u>L</u> <u>T</u> <u>Q</u> <u>D</u> <u>V</u> <u>R</u>	<u>VW</u> <u>V</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>H</u> <u>N</u> <u>G</u> <u>S</u> <u>M</u> <u>-</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>R</u> <u>G</u> <u>A</u> <u>F</u> <u>H</u> <u>L</u> <u>-</u> <u>A</u>	<u>V</u> <u>O</u> <u>A</u> <u>Q</u> <u>V</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>I</u>
Yeast LPAAT	201	<u>LEN</u> <u>V</u> <u>K</u> <u>K</u> <u>N</u> <u>K</u> <u>R</u> <u>A</u>	<u>LW</u> <u>V</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>Y</u> <u>T</u> <u>S</u> <u>E</u> <u>L</u> <u>T</u> <u>M</u> <u>L</u> <u>P</u> <u>F</u>	<u>KK</u> <u>G</u> <u>A</u> <u>F</u> <u>H</u> <u>L</u> <u>-</u> <u>A</u>	<u>Q</u> <u>Q</u> <u>G</u> <u>I</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>V</u>
E.coli LPAAT	201	<u>VN</u> <u>H</u> <u>F</u> <u>K</u> <u>K</u> <u>R</u> <u>R</u> <u>I</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u> <u>-</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> <u>-</u> <u>H</u> <u>A</u>	<u>I</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>
H.influenzae	201	<u>ARR</u> <u>I</u> <u>N</u> <u>E</u> <u>D</u> <u>N</u> <u>L</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u> <u>-</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> <u>T</u> <u>F</u> <u>H</u> <u>A</u>	<u>I</u> <u>S</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>
S.typhimurii	201	<u>VN</u> <u>H</u> <u>F</u> <u>K</u> <u>K</u> <u>R</u> <u>R</u> <u>I</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u> <u>-</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> <u>T</u> <u>F</u> <u>H</u> <u>A</u>	<u>I</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>
L.douglassi	201	<u>VR</u> <u>V</u> <u>I</u> <u>T</u> <u>E</u> <u>K</u> <u>N</u> <u>L</u> <u>S</u>	<u>L</u> <u>I</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>G</u> <u>D</u> <u>G</u> <u>R</u> <u>L</u> <u>-</u> <u>L</u> <u>P</u> <u>F</u>	<u>KK</u> <u>G</u> <u>F</u> <u>V</u> <u>H</u> <u>L</u> <u>-</u> <u>A</u>	<u>L</u> <u>Q</u> <u>S</u> <u>H</u> <u>L</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>M</u>
C. nucifera	201	<u>AR</u> <u>A</u> <u>W</u> <u>K</u> <u>K</u> <u>N</u> <u>L</u> <u>S</u>	<u>L</u> <u>I</u> <u>I</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>K</u> <u>T</u> <u>G</u> <u>R</u> <u>L</u> <u>-</u> <u>L</u> <u>P</u> <u>F</u>	<u>KK</u> <u>G</u> <u>F</u> <u>T</u> <u>H</u> <u>F</u> <u>T</u> <u>I</u> <u>A</u>	<u>L</u> <u>Q</u> <u>T</u> <u>R</u> <u>L</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>M</u>
	260	270	280	290	300	
Human LPAAT-β	251	<u>VY</u> <u>S</u> <u>S</u> <u>F</u> <u>S</u> <u>-</u> <u>F</u>	<u>Y</u> <u>N</u> <u>T</u> <u>K</u> <u>K</u> <u>F</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>T</u> <u>V</u> <u>I</u> <u>V</u> <u>Q</u> <u>V</u> <u>L</u> <u>E</u> <u>A</u>	<u>I</u> <u>P</u> <u>T</u> <u>S</u> <u>G</u> <u>L</u> <u>T</u> <u>A</u> <u>A</u> <u>D</u>	<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>V</u> <u>D</u> <u>T</u> <u>C</u> <u>H</u> <u>R</u>
Human LPAAT-α	251	<u>VM</u> <u>S</u> <u>S</u> <u>Y</u> <u>Q</u> <u>D</u> <u>-</u> <u>F</u>	<u>Y</u> <u>C</u> <u>K</u> <u>K</u> <u>E</u> <u>R</u> <u>R</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>Q</u> <u>Q</u> <u>V</u> <u>R</u> <u>V</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>P</u> <u>T</u> <u>E</u> <u>G</u> <u>L</u> <u>T</u> <u>P</u> <u>D</u> <u>D</u>	<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>A</u> <u>D</u> <u>R</u> <u>/</u> <u>R</u> <u>H</u>
Yeast LPAAT	251	<u>VS</u> <u>N</u> <u>I</u> <u>S</u> <u>T</u> <u>-</u> <u>L</u>	<u>V</u> <u>S</u> <u>P</u> <u>K</u> <u>Y</u> <u>G</u> <u>/</u> <u>F</u> <u>N</u> <u>R</u>	<u>G</u> <u>C</u> <u>M</u> <u>I</u> <u>V</u> <u>R</u> <u>I</u> <u>L</u> <u>K</u> <u>P</u>	<u>I</u> <u>S</u> <u>T</u> <u>E</u> <u>N</u> <u>L</u> <u>T</u> <u>K</u> <u>D</u> <u>K</u>	<u>I</u> <u>G</u> <u>E</u> <u>F</u> <u>A</u> <u>E</u> <u>K</u> <u>V</u> <u>R</u> <u>D</u>
E.coli LPAAT	251	<u>CV</u> <u>S</u> <u>T</u> <u>T</u> <u>S</u> <u>-</u> <u>-</u>	<u>N</u> <u>K</u> <u>I</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>I</u> <u>H</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>Q</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u> <u>C</u> <u>R</u> <u>-</u>
H.influenzae	251	<u>VC</u> <u>S</u> <u>S</u> <u>T</u> <u>H</u> <u>-</u> <u>-</u>	<u>N</u> <u>K</u> <u>I</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>W</u> <u>D</u> <u>N</u>	<u>G</u> <u>K</u> <u>V</u> <u>I</u> <u>C</u> <u>E</u> <u>I</u> <u>M</u> <u>D</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>G</u> <u>Y</u> <u>T</u> <u>K</u> <u>D</u> <u>N</u>	<u>V</u> <u>R</u> <u>D</u> <u>L</u> <u>A</u> <u>A</u> <u>Y</u> <u>C</u> <u>H</u> <u>F</u>
S.typhimurii	251	<u>CV</u> <u>S</u> <u>N</u> <u>I</u> <u>S</u> <u>-</u> <u>-</u>	<u>N</u> <u>K</u> <u>V</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>I</u> <u>N</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>D</u> <u>V</u> <u>S</u> <u>E</u> <u>X</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u> <u>C</u> <u>R</u> <u>F</u>
L.douglassi	251	<u>I</u> <u>L</u> <u>T</u> <u>G</u> <u>T</u> <u>H</u> <u>L</u> <u>A</u> <u>W</u> <u>F</u>	<u>T</u> <u>R</u> <u>K</u> <u>G</u> <u>I</u> <u>F</u> <u>R</u> <u>V</u> <u>R</u> <u>P</u>	<u>V</u> <u>P</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>N</u> <u>T</u> <u>D</u> <u>D</u> <u>T</u> <u>V</u> <u>D</u> <u>K</u>	<u>I</u> <u>D</u> <u>D</u> <u>Y</u> <u>V</u> <u>K</u> <u>M</u> <u>I</u> <u>H</u> <u>D</u>
C. nucifera	251	<u>VL</u> <u>T</u> <u>G</u> <u>T</u> <u>H</u> <u>L</u> <u>A</u> <u>W</u> <u>-</u>	<u>-</u> <u>R</u> <u>K</u> <u>N</u> <u>S</u> <u>L</u> <u>R</u> <u>V</u> <u>R</u> <u>P</u>	<u>A</u> <u>P</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>F</u> <u>S</u> <u>P</u>	<u>I</u> <u>K</u> <u>T</u> <u>D</u> <u>D</u> <u>W</u> <u>E</u> <u>E</u> <u>E</u> <u>K</u>	<u>I</u> <u>N</u> <u>H</u> <u>Y</u> <u>V</u> <u>E</u> <u>M</u> <u>I</u> <u>H</u> <u>F</u>

Figure 5D

	310	320	330	340	350
Human LPAAT-β	301 <u>AMRTTFIHIS</u> <u>KTPQENGATA</u> <u>GSGVQPAQ</u> *				
Human LPAAT-α	301 <u>SMLT¹VFREIS</u> <u>TDGRGGDYL</u> <u>KPGGGG</u> *				
Yeast LPAAT	301 <u>QMVDILKEIG</u> <u>YSPAINDTTL</u> <u>PFQAIEYAAL</u> <u>QHDKKVKKI</u> <u>KNEPVPSVSI</u>				
E.coli LPAAT	301 <u>-SIMEQKIAE</u> <u>LDKEVA</u> <u>-ER</u> <u>EAAGKV</u> *				
H.influenzae	301 <u>TILMEKRIAE</u> <u>LDEEIA</u> <u>-----</u> <u>KGN</u> *				
S.typhimuriu	301 <u>TALMEQKIAE</u> <u>LDKEVA</u> <u>-ER</u> <u>EATGKV</u> *				
L.douglassi	301 <u>IYVRNLPASQ</u> <u>KPLGS</u> <u>-TNR</u> <u>-S-K</u> *				
C. nucifera	301 <u>TALYVDHLPE</u> <u>SQKPLVSKGR</u> <u>DASGRNS</u> *				
	360	370	380	390	
Human LPAAT-β	351 -----				
Human LPAAT-α	351 -----				
Yeast LPAAT	351 <u>SNDVNT¹HN¹EG</u> <u>SSVKKMH</u> *				
E.coli LPAAT	351 -----				
H.influenzae	351 -----				
S.typhimuriu	351 -----				
L.douglassi	351 -----				
C. nucifera	351 -----				

Figure 9 A

TCTATGAAACCAACATACATGGCGTTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG	60
GGCAGGTGTCTGGCTTGTCCACCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGC	120
TGACCTTGTGCCTTGGACGGCTGTCCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGC	180
GCC ATG GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC	225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His	
5 10	
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC	270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn	
15 20 25	
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG	315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln	
30 35 40	
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC	360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser	
45 50 55	
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA	405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr	
60 65 70	
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC	450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His	
75 80 85	
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT	495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys	
90 95 100	
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG	540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys	
105 110 115	
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG	585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp	
120 125 130	
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG	630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu	
135 140 145	
GAG GAC CGG GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC	675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp	
150 155 160	
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC	720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg	
165 170 175	
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT	765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala	
180 185 190	
AAG GGG CTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG	810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys	
195 200 205	
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT	855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala	
210 215 220	
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC	900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC	945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys	
240 245 250	
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA	990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu	
255 260 265	
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC	1035

Figure 10 A

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCTCAACTGCCGCCTCGCC	61
TACTCACTCTGGAGCCTAGCACAAAACCTAGAAGCAACCCAAGCACCTGTCACTGGAGACT	121
AATTATGCGGCACCCATACAGGGACCCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTTAAAGCGAAAAAGGAAGTATACAACAAAGTCCATAACTGGTC ATG CTG	238
	Met Leu
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

Figure 10 B

	260		265		270		
CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT GTG GGA GCA GCT TCC							1093
Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser							
	275		280		285		
TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT GAG ATA GAA AAA GGC							1138
Phe Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly							
	290		295		300		
TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA AAG GAA TAA TTAATGGC							1185
Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu ***							
	305		310				
TGTGACTGAACACACGCGGCCCTGACGGTGGTATCCAGTTAACTCAAAACCAACACACAG							1245
AGTGCAGGAAAAGACAATTAGAACTATTTTTCTTATTAAGTGGTGACTAATATTAACAA							1305
AACTTGAGCCAAGAGTAAAGAATTCAGAAGGCCCTGTCAGGTGAAGTCTTCAGCCTCCAC							1365
AGCGCAGGGTCCCAGCATCTCCACGCGCGCCCGTGGGAGGTGGGTCCGGCCGGAGAGGCC							1425
TCCCGCGGACGCGTCTCTCCAGAACTCCGCTTCCAAGAGGGACCTTTGGCTGCTTTCTC							1485
TCCTTAAACTTAGATCAAATTTTAAAAAAAAAAAAAAAA							1523

Figure 11A

TGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAGGCTGCCAG	61
GAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACTGTGGG	121
TAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC ATG GAC CTC GCG GGA CTG	175
Met Asp Leu Ala Gly Leu	
5	
CTG AAG TCT CAG TTC CTG TGC CAC CTG GTC TTC TGC TAC GTC TTT	220
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe	
10 15 20	
ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC	265
Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe Thr Leu	
25 30 35	
CTC CTC TGG CCC ATT AAC AAG CAG CTC TTC CGG AAG ATC AAC TGC	310
Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys Ile Asn Cys	
40 45 50	
AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG CTG GAG	355
Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu	
55 60 65	
TGG TGG TCG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC GCC	400
Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala	
70 75 80	
TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC	445
Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His	
85 90 95	
AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC	490
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg	
100 105 110	
TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG	535
Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu	
115 120 125	
GCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAG ATG	580
Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met	
130 135 140	
GTC TTC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC	625
Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala	
145 150 155	
ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TAT TTT TTC	670
Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe	
160 165 170	
CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG	715
Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu	
175 180 185	
ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG	760
Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys	
190 195 200	
CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG	805
His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg	
205 210 215	
AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT	850
Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn	
220 225 230	
TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA	895
Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	
235 240 245	
AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA	940
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu	
250 255 260	
GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG	985
Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	
265 270 275	

Figure 11 B

[illegible]